10/043,615

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*** YOU HAVE NEW MAIL ***

=> s polymorphism/ti
L1        80380 POLYMORPHISM/TI

=> s l1 and modified base
L2           15 L1 AND MODIFIED BASE

=> s l2 and 90
L3            7 L2 AND 90

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4            7 DUP REM L3 (0 DUPLICATES REMOVED)

=> d l4 bib abs 1-7

L4   ANSWER 1 OF 7  USPATFULL on STN
AN     2005:137976  USPATFULL
TI     Single nucleotide polymorphism analysis of highly polymorphic
       target sequences
IN     Belousov, Yevgeniy, Mill Creek, CA, UNITED STATES
       Dempcy, Robert O., Kirkland, WA, UNITED STATES
       Lokhov, Sergey G., Kirkland, WA, UNITED STATES
       Vorobiev, Alexei, Redmond, WA, UNITED STATES
PA     Epoch Biosciences, Inc., Bothell, WA, UNITED STATES, 98021 (U.S.
       corporation)
PI     US 2005118623      A1   20050602
AI     US 2004-954955     A1   20040929 (10)
PRAI   US 2003-508792P     20031002 (60)
DT     Utility
FS     APPLICATION
LREP   TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH
       FLOOR, SAN FRANCISCO, CA, 94111-3834, US
CLMN   Number of Claims: 46
ECL    Exemplary Claim: 1
DRWN   10 Drawing Page(s)
LN.CNT 2692
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and probes are provided for the analysis of target sequences having two or more polymorphisms wherein one of the polymorphisms is to be distinguished and another polymorphism is to be masked.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 2 OF 7 USPATFULL on STN
AN 2004:292138 USPATFULL
TI P450 single nucleotide **polymorphism** biochip analysis
IN Chui, Buena, Chandler, AZ, UNITED STATES
Elghanian, Robert, Skokie, IL, UNITED STATES
Gupta, Vineet, Reading, MA, UNITED STATES
Jayaraman, Krishnamurthy, Hoffman Estates, IL, UNITED STATES
Kiser, Gretchen, Mesa, AZ, UNITED STATES
Li, Changming, Schaumburg, IL, UNITED STATES
Liu, Chang-Gong, Cherry Hill, NJ, UNITED STATES
Luehrsen, Kenneth R., Half Moon Bay, CA, UNITED STATES
Mazumder, Abhijit, Buffalo Grove, IL, UNITED STATES
Ramakrishnan, Ramesh, Vernon Hills, IL, UNITED STATES
Silbergleyt, Arkadiy, Chandler, AZ, UNITED STATES
Tuggle, Todd, Oceanside, CA, UNITED STATES
Yamashiro, Carl, Chandler, AZ, UNITED STATES
Yowanto, Handy, Walnut, CA, UNITED STATES
Pestova, Ekaterina, Downers Grove, IL, UNITED STATES
Fermin, David R., Minneapolis, MN, UNITED STATES
Wang, David G., Deerfield, IL, UNITED STATES
Gu, Zhijie John, San Diego, CA, UNITED STATES
PI US 2004229222 A1 20041118
AI US 2002-114908 A1 20020401 (10)
PRAI US 2001-280583P 20010330 (60)
DT Utility
FS APPLICATION
LREP DORSEY & WHITNEY LLP, Suite 3400, Four Embarcadero Center, San Francisco, CA, 94111-4187
CLMN Number of Claims: 48
ECL Exemplary Claim: 1
DRWN 44 Drawing Page(s)
LN.CNT 4516
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to methods and compositions for determining single nucleotide polymorphisms (SNPs) in P450 genes. In preferred embodiments, self extension of interrogation probes is prevented by using novel non self-extension probes and/or methods, thereby improving the specificity and efficiency of P450 SNP detection in target samples with minimal false positive results. The invention thus describes a variety of methods to decrease self-extension of interrogation probes. In addition, this invention provides a unique collection of P450 SNP probes on one assay, primer sequences for specific amplification of each of the seven P450 genes and amplicon control probes to evaluate whether the intended p450 gene targets were amplified successfully. The invention also describes a variety of array platforms for performing the assays of the invention; for example: CodeLink.TM., eSensor.TM., multiplex arrays with cartridges etc., all described herein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 3 OF 7 USPATFULL on STN
AN 2004:50854 USPATFULL
TI Method of screening for genetic **polymorphism**
IN Brenner, Sydney, Cambridge, UNITED KINGDOM
PA Lynx Therapeutics, Inc. (non-U.S. corporation)
PI US 2004038283 A1 20040226
AI US 2003-646451 A1 20030821 (10)
RLI Division of Ser. No. US 2001-786254, filed on 30 Apr 2001, GRANTED, Pat. No. US 6653077
DT Utility
FS APPLICATION

LREP PERKINS COIE LLP, P.O. BOX 2168, MENLO PARK, CA, 94026
CLMN Number of Claims: 16
ECL Exemplary Claim: 1
DRWN 4 Drawing Page(s)
LN.CNT 777
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Method and materials are provided for screening for genetic polymorphism in a test population of DNA fragments. Heteroduplexes are formed between members a test DNA population and their corresponding complements from a reference DNA population. Perfectly matched heteroduplexes are destroyed or separated from those containing mismatched sequences. Preferably, perfectly matched heteroduplexes are digested by a single stranded exonuclease which requires double stranded DNA as a substrate, such as E. coli exonuclease III. Amplicons are formed from mismatched heteroduplexes, preferably by extending the partially digested duplexes after treatment with exonuclease III followed by PCR amplification. The resulting amplicons are inserted into a cloning vector which is used to transform a bacterial host. After host cells are plated and allowed to form colonies, clones are picked and sequenced to identify DNA fragments containing polymorphic sequences.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 4 OF 7 USPATFULL on STN
AN 2003:257695 USPATFULL
TI **Polymorphism** detection and separation
IN Kmiec, Eric B., Landenberg, PA, UNITED STATES
Rice, Michael C., Newton, PA, UNITED STATES
PI US 2003180746 A1 20030925
AI US 2002-260150 A1 20020927 (10)
RLI Continuation-in-part of Ser. No. WO 2002-US9691, filed on 27 Mar 2002, PENDING
PRAI US 2001-325992P 20010927 (60)
US 2001-325828P 20010928 (60)
DT Utility
FS APPLICATION
LREP FISH & NEAVE, 1251 AVENUE OF THE AMERICAS, 50TH FLOOR, NEW YORK, NY, 10020-1105
CLMN Number of Claims: 108
ECL Exemplary Claim: 1
DRWN 31 Drawing Page(s)
LN.CNT 4903
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions for polymorphism detection and separation. The methods are readily multiplexed, can be adapted to a variety of existing detection systems, and permit target amplification without PCR. The methods permit allelic variants selectively to be isolated, with or without contemporaneous detection, and finds particular utility in facilitating the construction of coisogenic cell collections in which the cells differ genotypically by single nucleotide changes targeted to defined loci.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 5 OF 7 USPATFULL on STN
AN 2003:308986 USPATFULL
TI Method of screening for genetic **polymorphism**
IN Brenner, Sydney, Cambridge, UNITED KINGDOM
PA Lynx Therapeutics, Inc., Hayward, CA, United States (U.S. corporation)
PI US 6653077 B1 20031125
WO 2000014282 20000316
AI US 2001-786254 20010430 (9)
WO 1999-US20047 19990831
PRAI US 1998-99147P 19980904 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Myers, Carla J.
LREP Dehlinger, Peter J., Gorthey, Lee Ann, Perkins Coie LLP

CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN 4 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 727
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Method and materials are provided for screening for genetic polymorphism in a test population of DNA fragments. Heteroduplexes are formed between members of a test DNA population and their corresponding complements from a reference DNA population. Perfectly matched heteroduplexes are destroyed or separated from those containing mismatched sequences. Preferably, perfectly matched heteroduplexes are digested by a single stranded exonuclease which requires double stranded DNA as a substrate, such as E. coli exonuclease III. Amplicons are formed from mismatched heteroduplexes, preferably by extending the partially digested duplexes after treatment with exonuclease III followed by PCR amplification. The resulting amplicons are inserted into a cloning vector which is used to transform a bacterial host. After host cells are plated and allowed to form colonies, clones are picked and sequenced to identify DNA fragments containing polymorphic sequences.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 6 OF 7 USPATFULL on STN
AN 2002:280033 USPATFULL
TI Method for the determination of at least one functional **polymorphism** in the nucleotide sequence of a preselected candidate gene and its applications
IN Escary, Jean-Louis, Le Chesnay, FRANCE
PI US 2002155467 A1 20021024
AI US 2001-10749 A1 20011206 (10)
PRAI FR 2000-15838 20001206
DT Utility
FS APPLICATION
LREP Mark A. Hofer, Brown, Rudnick, Freed & Gesmer, One Financial Center, Boston, MA, 02111
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 4 Drawing Page(s)
LN.CNT 2153
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention concerns a method for determining at least one functional SNP in a gene, comprising preselecting a candidate gene, providing a sample population comprising a significant number of individuals chosen substantially at random from the general population, isolating from each individual of the sample population at least one fragment of the nucleotide sequence of the preselected candidate gene, identifying at least one SNP in at least one fragment and determining the functionality of said SNP(s). The present invention also concerns applications of this method.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 7 OF 7 USPATFULL on STN
AN 2000:24452 USPATFULL
TI Diagnostic assays and kits for body mass disorders associated with a **polymorphism** in an intron sequence of the SR-BI gene
IN Acton, Susan Laurene, Lexington, MA, United States
Ordovas, Jose M., Framingham, MA, United States
PA Millennium Pharmaceuticals, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6030778 20000229
AI US 1997-890979 19970710 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Arthur, Lisa B.
LREP Foley, Hoag & Eliot LLC, Arnold, Esq., Beth E., Clauss, Isabelle M.
CLMN Number of Claims: 28
ECL Exemplary Claim: 1

DRWN 10 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 2717
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is based at least in part on the discovery of a polymorphism in the human SR-BI gene which is genetically linked with a high body mass index. Accordingly, the invention provides diagnostic assays and kits for determining whether a subject has or is at risk of developing an abnormal body mass index, such as a high body mass.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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